

SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
THEREFOR

<130> HAR-005

<140> 09/248,964
<141> 1999-02-12

<150> PCT/US97/14503
<151> 1997-08-15

<150> 60/075,351
<151> 1998-02-19

<150> 60/024,007
<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: DR2-Fos fusion

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<220>
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<222> (1)..(21)
<223> 3' end of secretory signal

<220>
<221> misc_structure
<222> (22)..(594)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (595)..(615)
<223> Linker sequence

<220>
<221> misc_feature
<222> (616)..(735)
<223> Fos leucine zipper domain



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TC 1700 MAIL ROOM

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gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac	96
Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp	
20 25 30	
ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg	144
Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr	
35 40 45	
gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa	192
Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln	
50 55 60	
ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg	240
Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met	
65 70 75 80	
aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta	288
Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val	
85 90 95	
act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc	336
Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu	
100 105 110	
atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg	384
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp	
115 120 125	
ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc	432
Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe	
130 135 140	
ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc	480
Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe	
145 150 155 160	
ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc	528
Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly	
165 170 175	
ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct	576
Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro	
180 185 190	
ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat	624
Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp	
195 200 205	
aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg	672
Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu	
210 215 220	

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cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720
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 Ile Leu Ala Ala His
 245

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DR2-Fos fusion

<220>
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 <223> 3' end of secretory signal

<220>
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 <222> (8)..(198)
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 <222> (199)..(205)
 <223> Linker sequence

<220>
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 <222> (206)..(245)
 <223> Fos leucine zipper domain

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 20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
 35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
 50 55 60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65 70 75 80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
 85 90 95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
 100 105 110

Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
 115 120 125
 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
 130 135 140
 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
 145 150 155 160
 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
 165 170 175
 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
 180 185 190
 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
 195 200 205
 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
 210 215 220
 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
 225 230 235 240
 Ile Leu Ala Ala His
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<213> Artificial Sequence

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<220>

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<222> (1)..(21)

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<221> misc_feature

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<223> DRB1*1501 extracellular domain

<220>

<221> misc_feature

<222> (616)..(636)

<223> Linker sequence

<220>

<221> misc_feature

<222> (637)..(756)

<223> Jun leucine zipper domain

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cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg	96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg	
20 25 30	
ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac	144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp	
35 40 45	
agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac	192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp	
50 55 60	
gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc	240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala	
65 70 75 80	
gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc	288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe	
85 90 95	
aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag	336
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys	
100 105 110	
acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt	384
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly	
115 120 125	
ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa	432
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu	
130 135 140	
gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg	480
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp	
145 150 155 160	
acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag	528
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu	
165 170 175	
gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca	576
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr	
180 185 190	
gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga	624
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly	
195 200 205	

ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg 672
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa 720
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 225 230 235 240

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 20 25 30

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 35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
 50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
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Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
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<213> Artificial Sequence

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42

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 6
gtcatagaat tctcaatggg cggccaggat gaactccag

39

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 7
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<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 8
gtcatagaat totcaatggt tcatgacttt ctgtttaag 39

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
biotin ligase recognition sequence

<400> 9
Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
1 5 10

<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic,
linker sequence

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<210> 11
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<212> DNA
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<222> (610)..(729)
<223> Fos leucine zipper domain

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<222> (730)..(1437)
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ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

ggg gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 144
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 192
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag 240
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg	288
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val	
85 90 95	
ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt	336
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys	
100 105 110	
ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga	384
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg	
115 120 125	
aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc	432
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro	
130 135 140	
agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc	480
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro	
145 150 155 160	
tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat	528
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp	
165 170 175	
gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca	576
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro	
180 185 190	
gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc	624
Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu	
195 200 205	
caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc	672
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr	
210 215 220	
gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg	720
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu	
225 230 235 240	
gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt	768
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys	
245 250 255	
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc	816
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val	
260 265 270	
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc	864
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser	
275 280 285	
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat	912
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp	
290 295 300	

gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag	960
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln	
305 310 315 320	
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt	1008
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser	
325 330 335	
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa	1056
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys	
340 345 350	
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc	1104
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile	
355 360 365	
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct	1152
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro	
370 375 380	
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg	1200
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met	
385 390 395 400	
gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac	1248
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn	
405 410 415	
ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct	1296
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser	
420 425 430	
gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac	1344
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn	
435 440 445	
tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg	1392
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu	
450 455 460	
cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa	1437
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys	
465 470 475	
tgagaattc	1446

<210> 12

<211> 479

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: DR2-IgG fusion

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<223> IgG domain

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Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp

165							170						175			
Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	Leu	Pro	
			180				185						190			
Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu	Thr	Asp	Thr	Leu	
			195				200						205			
Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser	Ala	Leu	Gln	Thr	
			210				215						220			
Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu	Glu	Phe	Ile	Leu	
			225				230						235			
Ala	Ala	His	Ala	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	
			245				250						255			
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	
			260				265						270			
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	
			275				280						285			
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	
			290				295						300			
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	
			305				310						315			
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	
			325				330						335			
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	
			340				345						350			
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	
			355				360						365			
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	
			370				375						380			
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	
			385				390						395			
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	
			405				410						415			
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	
			420				425						430			
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	
			435				440						445			
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	
			450				455						460			
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465

470

475

<210> 13

<211> 1851

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> CDS

<222> (1)..(1836)

<220>

<221> misc_feature

<222> (1)..(75)

<223> 3' end of secretory signal

<220>

<221> misc_feature

<222> (76)..(648)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (649)..(669)

<223> Linker

<220>

<221> misc_feature

<222> (670)..(789)

<223> Fos leucine zipper domain

<220>

<221> misc_feature

<222> (790)..(1836)

<223> IgG domain

<400> 13

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val

1

5

10

15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile

20

25

30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met

35

40

45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys

50

55

60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta	672
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu	
210 215 220	
act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct	720
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser	
225 230 235 240	
gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg	768
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu	
245 250 255	
gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat	816
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn	
260 265 270	
gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag	864
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys	
275 280 285	
tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca	912

Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr	
290						295					300					
gta	tcc	tgg	cta	aag	gat	ggg	aag	ctc	gtg	gaa	tct	ggc	ttc	acc	aca	960
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr	
305					310					315					320	
gat	ccg	gtg	acc	atc	gag	aac	aaa	gga	tcc	aca	ccc	caa	acc	tac	aag	1008
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys	
				325					330					335		
gtc	ata	agc	aca	ctt	acc	atc	tct	gaa	atc	gac	tgg	ctg	aac	ctg	aat	1056
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn	
			340					345					350			
gtg	tac	acc	tgc	cgt	gtg	gat	cac	agg	ggg	ctc	acc	ttc	ttg	aag	aac	1104
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn	
		355					360					365				
gtg	tcc	tcc	aca	tgt	gct	gcc	agt	ccc	tcc	aca	gat	atc	ctt	aat	ttt	1152
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe	
	370					375					380					
act	att	cct	cct	tcc	ttt	gcc	gac	atc	ttc	ctt	agc	aag	tcc	gct	aac	1200
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn	
385					390					395					400	
ctg	acc	tgt	ctg	gtc	tca	aac	ctg	gca	acc	tat	gaa	acc	ctg	agt	atc	1248
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile	
				405					410						415	
tcc	tgg	gct	tct	caa	agt	ggg	gaa	cca	ctg	gaa	acc	aaa	att	aaa	atc	1296
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile	
			420					425					430			
atg	gaa	agc	cat	ccc	aat	ggc	acc	ttc	agt	gct	aag	ggg	gtg	gct	agt	1344
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser	
		435					440					445				
gtt	tgt	gtg	gaa	gac	tgg	aat	aac	agg	aag	gaa	ttt	gtg	tgt	act	gtg	1392
Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val	
	450					455					460					
act	cac	agg	gat	ctg	cct	tca	cca	cag	aag	aaa	ttc	atc	tca	aaa	ccc	1440
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro	
465					470					475					480	
aat	gag	gtg	cac	aaa	cat	cca	cct	gct	gtg	tac	ctg	ctg	cca	cca	gct	1488
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala	
				485					490					495		
cgt	gaa	caa	ctg	aac	ctg	agg	gag	tca	gcc	aca	gtc	acc	tgc	ctg	gtg	1536
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val	
			500					505					510			
aag	ggc	ttc	tct	cct	gca	gac	atc	tct	gtg	caa	tgg	aag	cag	agg	ggc	1584
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly	

515	520	525	
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag	1632		
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu			
530	535	540	
cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca	1680		
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr			
545	550	555	560
gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac	1728		
Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His			
565	570	575	
gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act	1776		
Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr			
580	585	590	
ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc	1824		
Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly			
595	600	605	
ggc acc tgc tat tgaagatctg togac	1851		
Gly Thr Cys Tyr			
610			

<210> 14
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DR2-IgM fusion

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> 3' end of secretory signal

<220>
 <221> misc_feature
 <222> (26)..(216)
 <223> DRA*0101 extracellular domain

<220>
 <221> misc_feature
 <222> (217)..(223)
 <223> Linker

<220>
 <221> misc_feature
 <222> (224)..(263)
 <223> Fos leucine zipper domain

<220>
 <221> misc_feature
 <222> (264)..(612)

<223> IgG domain

<400> 14

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
20 25 30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu
210 215 220

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225 230 235 240

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
245 250 255

Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
260 265 270

Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
275 280 285

Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr	290	295	300
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr	305	310	315
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys	325	330	335
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn	340	345	350
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn	355	360	365
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe	370	375	380
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn	385	390	395
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile	405	410	415
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile	420	425	430
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser	435	440	445
Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val	450	455	460
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro	465	470	475
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala	485	490	495
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val	500	505	510
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly	515	520	525
Gln	Leu	Leu	Pro	Gln	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	530	535	540
Pro	Gly	Ala	Pro	Gly	Phe	Tyr	Phe	Thr	His	Ser	Ile	Leu	Thr	Val	Thr	545	550	555
Glu	Glu	Glu	Trp	Asn	Ser	Gly	Glu	Thr	Tyr	Thr	Cys	Val	Val	Gly	His	565	570	575
Glu	Ala	Leu	Pro	His	Leu	Val	Thr	Glu	Arg	Thr	Val	Asp	Lys	Ser	Thr	580	585	590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610